



## RAW SEQUENCE LISTING

DATE: 05/30/2003

PATENT APPLICATION: US/09/892,316

TIME: 12:18:52

Input Set : N:\CrF3\RULE60\09892316.RAW.txt

Output Set: N:\CRF4\05302003\I892316.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Hillman, Jennifer L.

6 Goli, Surya K.

8 (ii) TITLE OF INVENTION: HUMAN LEA-MOTIF DEVELOPMENTAL

9 PROTEIN

11 (iii) NUMBER OF SEQUENCES: 3

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

15 (B) STREET: 3174 Porter Drive

16 (C) CITY: Palo Alto

17 (D) STATE: CA

18 (E) COUNTRY: USA

19 (F) ZIP: 94304

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Diskette

23 (B) COMPUTER: IBM Compatible

24 (C) OPERATING SYSTEM: DOS

25 (D) SOFTWARE: FastSEQ for Windows Version 2.0

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/892,316

C--> 29 (B) FILING DATE: 30-May-2003

30 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US/08/796,676

35 (B) FILING DATE:

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Billings, Lucy J.

40 (B) REGISTRATION NUMBER: 36,749

41 (C) REFERENCE/DOCKET NUMBER: PF-0213 US

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: 415-855-0555

45 (B) TELEFAX: 415-845-4166

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 219 amino acids

52 (B) TYPE: amino acid

53 (C) STRANDEDNESS: single

54 (D) TOPOLOGY: linear

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

59 Met Val Lys Tyr Phe Leu Gly Gln Ser Val Leu Arg Ser Ser Trp Asp

60 1 5 10 15

61 Gln Val Phe Ala Ala Phe Trp Gln Arg Tyr Pro Asn Pro Tyr Ser Lys

ENTERED

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62		20		25		30
63	His Val Leu Thr Glu Asp Ile Val His Arg Glu Val Thr Pro Asp Gln					
64		35		40		45
65	Lys Leu Leu Ser Arg Arg Leu Leu Thr Lys Thr Asn Arg Met Pro Arg					
66		50		55		60
67	Trp Ala Glu Arg Leu Phe Pro Ala Asn Val Ala His Ser Val Tyr Val					
68		65		70		75
69	Leu Glu Asp Ser Ile Val Asp Pro Gln Asn Gln Thr Met Thr Thr Phe					
70		85		90		95
71	Thr Trp Asn Ile Asn His Ala Arg Leu Met Val Val Glu Glu Arg Cys					
72		100		105		110
73	Val Tyr Cys Val Asn Ser Asp Asn Ser Gly Trp Thr Glu Ile Arg Arg					
74		115		120		125
75	Glu Ala Trp Val Ser Ser Ser Leu Phe Gly Val Ser Arg Ala Val Gln					
76		130		135		140
77	Glu Phe Gly Leu Ala Arg Phe Lys Ser Asn Val Thr Lys Thr Met Lys					
78		145		150		155
79	Gly Phe Glu Tyr Ile Leu Ala Lys Leu Gln Gly Glu Ala Pro Ser Lys					
80		165		170		175
81	Thr Leu Val Glu Thr Ala Lys Glu Ala Lys Glu Lys Ala Lys Glu Thr					
82		180		185		190
83	Ala Leu Ala Ala Thr Glu Lys Ala Lys Asp Leu Ala Ser Lys Ala Ala					
84		195		200		205
85	Thr Lys Lys Gln Gln Gln Gln Gln Phe Val					
86		210		215		

## 88 (2) INFORMATION FOR SEQ ID NO: 2:

## 90 (i) SEQUENCE CHARACTERISTICS:

91 (A) LENGTH: 858 base pairs

92 (B) TYPE: nucleic acid

93 (C) STRANDEDNESS: single

94 (D) TOPOLOGY: linear

## 97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

99	GCGGTGGTGA CTGAGCTACG AGCCTGGCGG CGGGTGTGCG CCGAGCCCCG GCCCGGCCCG	60
100	GCCCTCGCGT GCCTCCAGG CTCCGCACCC CTGATGCTGC GCGGGTGCTG AGCCCGCTTC	120
101	GGCCGGGACG ATGGTGAAGT ATTTCTTGGG CCAGAGCGTG CTCCGGAGTT CCTGGGACCA	180
102	AGTGTTGCGC GCCTTCTGGC AGCGGTACCC GAATCCCTAT AGCAAACATG TCTTGACGGA	240
103	AGACATAGTA CACCGGGAGG TGACCCCTGA CCAGAACTG CTGTCCCGGC GACTCCTGAC	300
104	CAAGACCAAC AGGATGCCAC GCTGGGCCGA GCGACTATTT CCTGCCAATG TTGCTCACTC	360
105	GGTGTACGTC CTGGAGGACT CTATTGTGGA CCCACAGAAT CAGACCATGA CTACCTTCAC	420
106	CTGGAACATC AACCACGCCC GGCTGATGGT GGTGGAGGAA CGATGTGTTT ACTGTGTGAA	480
107	CTCTGACAAC AGTGGCTGGA CTGAAATCCG CCGGGAAGCC TGGGTCTCCT CTAGCTTATT	540
108	TGGTGTCTCC AGAGCTGTCC AGGAATTTGG TCTTGCCCGG TTCAAAAAGCA ACGTGACCAA	600
109	GACTATGAAG GGTTTTGAAT ATATCTTGGC TAAGCTGCAA GGCGAGGCC CTTCCAAAAC	660
110	ACTTGTGAG ACAGCCAAGG AAGCCAAGGA GAAGGCAAAG GAGACGGCAC TGGCAGCTAC	720
111	AGAGAAGGCC AAGGACCTCG CCAGCAAGGC GGCCACCAAG AAGCAGCAGC AGCAGCAACA	780
112	GTTTGTGTAG CCAGTCTACC ACCACCACAG CACCCACAGC AGCTAGGCTT AGCCCTCTG	840
113	CCCTCCCTTC ATTGTACT	858

## 115 (2) INFORMATION FOR SEQ ID NO: 3:

## 117 (i) SEQUENCE CHARACTERISTICS:

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118      (A) LENGTH: 215 amino acids
119      (B) TYPE: amino acid
120      (C) STRANDEDNESS: single
121      (D) TOPOLOGY: linear
123      (vii) IMMEDIATE SOURCE:
124          (A) LIBRARY: GenBank
125          (B) CLONE: 969170
127      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
129      Met Gly Lys Tyr Cys Ala Ser Leu Gly Val Leu Lys Gly Pro Trp Asp
130      1      5      10      15
131      Gln Val Phe Ala Ala Phe Trp Gln Arg Tyr Pro Asn Pro Tyr Ser Lys
132      20      25      30
133      His Val Leu Thr Glu Asp Ile Val His Arg Glu Val Thr Ala Asp His
134      35      40      45
135      Lys Leu Leu Ser Arg Arg Leu Leu Thr Lys Thr Asn Arg Met Pro Arg
136      50      55      60
137      Trp Ala Glu Arg Phe Phe Pro Ala Asn Val Ala His Asn Val Tyr Ile
138      65      70      75      80
139      Val Glu Asp Ser Ile Val Asp Pro Lys Asn Arg Thr Met Thr Thr Phe
140      85      90      95
141      Thr Trp Asn Ile Asn His Ala Arg Leu Met Ala Val Glu Glu Arg Cys
142      100     105     110
143      Val Tyr Arg Val Asn Pro Glu Asn Ser Ser Trp Thr Glu Val Lys Arg
144      115     120     125
145      Glu Ala Trp Val Ser Ser Ser Leu Phe Gly Val Ser Arg Ala Val Gln
146      130     135     140
147      Glu Phe Gly Leu Ala Arg Phe Lys Ser Asn Val Thr Lys Ser Thr Lys
148      145     150     155     160
149      Gly Phe Glu Tyr Val Leu Ala Arg Met Gln Gly Glu Ala Pro Ser Lys
150      165     170     175
151      Thr Leu Val Glu Thr Ala Lys Glu Ala Thr Glu Lys Ala Lys Glu Thr
152      180     185     190
153      Ala Leu Ala Ala Thr Glu Lys Ala Lys Asp Leu Ala Ser Lys Ala Ala
154      195     200     205
155      Thr Lys Lys Lys Gln Phe Val
156      210     215

```

**VERIFICATION SUMMARY**

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]